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#4 / K.T.

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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/974,546**

DATE: 12/18/2001  
TIME: 16:40:03

Input Set : N:\CrF3\RULE60\09974546.raw  
Output Set: N:\CRF3\12182001\I974546.raw

## **SEQUENCE LISTING**

ENTERED

RAW SEQUENCE LISTING  
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TIME: 16:40:03

Input Set : N:\Crf3\RULE60\09974546.raw  
Output Set: N:\CRF3\12182001\I974546.raw

68 ATTATCTTGA AATGCCATT CATCTCCACA TTTGCTGTAG GCAGTAGTT AGTGGGTCCA 360  
 70 TTATATCTGC CACACTGATT GTCTTAAATA A 391  
**RECEIVED**  
 73 (2) INFORMATION FOR SEQ ID NO: 2:  
 75 (i) SEQUENCE CHARACTERISTICS:  
 76 (A) LENGTH: 614 base pairs JAN 08 2002  
 77 (B) TYPE: nucleic acid  
 78 (C) STRANDEDNESS: single TECH CENTER 1600/2900  
 79 (D) TOPOLOGY: linear  
 81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 83 CAGTAGTGGC CCCAAATGCC AGGCTGCACT GATATTATT GGATATAAGA CAAAGGGCA 60  
 85 GGGTAAGGAA TGTGAACCCT CTCCAATAAT AGGTAAGGTC ACATGGGTCA TGTGTCCACT 120  
 87 GGACAGGGGG CCCTTCCCTG CCTGGCAGCA GAGGCAGAGA GAGAGAGAGAGAC 180  
 89 AGCTTATGCC ATTATTCTG CATATCAGAC ATTTAGTACT TTCACTAATT TGCTCCTGCT 240  
 91 ATCTAAAAGG CAGAGCCAGG TATACAGGAT GGAACATGAA AGCGGACTAG GAGCGTGACC 300  
 93 ACTGAAGCAC AGCATCACAG GGAGACAGGC CTCTGGATAC TGGCCGGGGG GCCCTGACTG 360  
 95 ATGTCAAGGC CCTCCACAAG AGTGGAGGAG TTAGTCTTCC TCTAAACTCC CCCGGGGAA 420  
 97 AGGGAGGCTC CTTTCCCAG TCTGCTAAGT AGTGGGTGTT TTTCCTTGAC ACTGATGCTA 480  
 99 CTGCTAGACC ATGGTCCACT TTGCAACAGG CATCTCCCA GACACTGGTG TTACTGCTAG 540  
 101 ACCAACGCCCT CTGGTGGCCC TGTCCGGCA TAAGAGAAGG CTCACACTCT TGTCTTCTGG 600  
 103 CCACTTCGCA CTAT 614  
 106 (2) INFORMATION FOR SEQ ID NO: 3:  
 108 (i) SEQUENCE CHARACTERISTICS:  
 109 (A) LENGTH: 757 base pairs  
 110 (B) TYPE: nucleic acid  
 111 (C) STRANDEDNESS: single  
 112 (D) TOPOLOGY: linear  
 114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 116 ACAACGACAC ATTCAAGGAGT TAAATATTAA TCATCAAACA TTGGATTTT CCTTAACGCT 60  
 118 AGAGATTGCT ACAAACTTC TGAAGGGTCT CAATGGCTTC AGGCTAAGAA GAGATTCTC 120  
 120 CCTGTTATAA GCAGCAAGAC AAATTAGCCA TTTCACTCTC AAACCTCACT AATGATCACA 180  
 122 TTCTTCCAA AAGGAACCT AGAAGACCAA ATGCCCGAG TTAAGAACAT CAAAACAAAC 240  
 124 CATCTGAAGA AACCTCCAA GTGTAAGACT CTGCCATTAA AACATTACCG AGAGGGACT 300  
 126 CAAACAGTCT TTTCTCCCT TTGTCGTGTT TCTTGCTCC CAGACCCAAG GCACTTGGCG 360  
 128 GACAGTACTT GATACAATAA TTTAAAAAGC ACCACTCCCT TCCCACTTG TAAATACCA 420  
 130 GAACTCTAAT TGGACCACCC TGAAGCTTAG GACCTACCAAG CCATACAAAT AGTAAACTCT 480  
 132 GTCCACGATT CACTCATCTG TGTATTTCT ATAGATGTT ACTAGGCCTT TGTTATATAA 540  
 134 AAATACCCCG GCCAGGCACG GTGGCTCACG CCTGTAATCC CAGCACTTG GGAGGTGGGT 600  
 136 GGATCACCTG AGGTGGGAG TTCGAGACCA GCCTGACCAG CATGGTGAA CCCCCATCTC 660  
 138 TACTAAAAAC ACAAAAAATT AGCCGGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC 720  
 140 AGGAGGCTGA GGCGGAGAAT TGCTGAACC CGGAAGG 757  
 143 (2) INFORMATION FOR SEQ ID NO: 4:  
 145 (i) SEQUENCE CHARACTERISTICS:  
 146 (A) LENGTH: 673 base pairs  
 147 (B) TYPE: nucleic acid  
 148 (C) STRANDEDNESS: single  
 149 (D) TOPOLOGY: linear  
 151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 153 CAGGACACAG AGTAAGATAC CCACTGACTT CTTGTTGCT ACTTCCTGGG TGTTGTTCA 60  
 155 ATGGGCTTTG TTATAACAGG ACTAGTCTTC TGTAAATACA ACTTGGTAAA TAGGATGAAA 120

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157	CATAACTTTG CGACAATTCA GTAGAAATAG GCATACAAAC CTGGGCCTGA TGACACTCAC	180
159	CTCCCCTTGG CTATAAACAT TACCCTACCT GTTAAGTCAG TAATCCTTG GGAGAGCGCT	240
161	TACTGAGTAT CTATGATATG CAAAGACCAA AGACCGAGGG GGATCCCTGG TGAGAGCAA	300
163	GCACACACCT GGTTATTAGC TACCTGCCAC CCTGCTGGC ATGCAACATA CATTGTCTCA	360
165	AATTCTAAC ACCCTGCAAG GCAAGCTTCC TTGTTCTTT AAAGAAGAAA AGTAGACCAG	420
167	CAAGATTGAT TTGCTCAAGA TTACACAGCC TGGAATCTTG TCATGGGCAT GTCTGACTCT	480
169	GATAGCAATA CCCTCAAAGA AACTGTCAGA GAAGACTCAA TAAGAAGAAA GTTGAGATAC	540
171	AGAAACCAAC AGGAGAAGGT AATTCAAGAAA TTCAACACAGA GTGGGTGTGA TGGGAAGAAT	600
173	TCATTAATAA GAAGGTACCT CTGTAGAAAA ATCTTACCAAG ACAGTCTGGA AGTGAAGGAA	660
175	ACAGCCAATA GTC	673
178	(2) INFORMATION FOR SEQ ID NO: 5:	
180	(i) SEQUENCE CHARACTERISTICS:	
181	(A) LENGTH: 358 base pairs	
182	(B) TYPE: nucleic acid	
183	(C) STRANDEDNESS: single	
184	(D) TOPOLOGY: linear	
186	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
188	GTCACTGCAC ATTAAGATGG AGCCCGAAGA GCCACACTCC GAGGGGGCAT CGCAGGAGGA	60
190	TGGGGCTCAA GGTGCCTGGG GCTGGGCACC CCTAAGTCAC GGCTCTAAGG AGAAAGCTCT	120
192	CTTCCTGCCCG GGCAGAGCCC TCCCCCTCCCC CCGGATCCCC GTGCTTCCC GAGAGGGGAG	180
194	GACCAGAGAC CGGCAGATGG CTGCAGCGCT CCTCACTGCC TGTTCCCAGA TGCCAGTGAC	240
196	TTTCGAGGAT GTGGCCTTGT ACCTCTCCCG GGAGGAGTGG GGACGGCTGG ACCACACGCA	300
198	GCAGAACTTC TACAGGAAT GTCCTGCAGA AGAAAATGG GCTGTCACTG GGCTTCC	358
201	(2) INFORMATION FOR SEQ ID NO: 6:	
203	(i) SEQUENCE CHARACTERISTICS:	
204	(A) LENGTH: 23 base pairs	
205	(B) TYPE: nucleic acid	
206	(C) STRANDEDNESS: single	
207	(D) TOPOLOGY: linear	
209	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
211	CACAGATGTA GCTTCCTCAC TGG	23
214	(2) INFORMATION FOR SEQ ID NO: 7:	
216	(i) SEQUENCE CHARACTERISTICS:	
217	(A) LENGTH: 610 base pairs	
218	(B) TYPE: nucleic acid	
219	(C) STRANDEDNESS: single	
220	(D) TOPOLOGY: linear	
222	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
224	CTGGAGTACA ATGTCAGTGT TTACACTGTC AAGGATGACA AGGAAAGTGT CCCATCTCT	60
226	GATACCCTCA TCCCAGCTGT TCCTCCTCCC ACTGACCTGC GATTCAACAA CATGGTCCA	120
228	GACACCATGC GTGTACCTG GGCTCCACCC CCATCCATTG ATTTAACCAA CTTCTGGTG	180
230	CGTTACTCAC CTGTAAAAA TGAGGAAGAT GTTGCAGAGT TGTCAATTTC TCCTTCAGAC	240
232	AATGCACTGG TCTTAACAAA TCTCCTGCCT GGTACAGAAT ATGTAAGTGAG TGTCTCCAGT	300
234	GTCTACGAAC AACATGAGAG CACACCTCTT AGAGGAAGAC AGAAAACAGG TCTTGATTCC	360
236	CCAACTGGCA TTGACTTTTC TGATATTACT GCCAACTCTT TTACTGTGCA CTGGATTGCT	420
238	CCTCGAGCCA CCATCACTGG CTACAGGATC CGCCATCATC CCGAGCACTT CAGTGGGAGA	480
240	CCTCGAGAAG ATCGGGTGCCT CCACCTCTGG AATTCCATCA CCCTCACCAA CCTCACTCCA	540
242	GGCACAGAGT ATGTCAGTGT CATCGTTGCT CTTAATGGCA GAGAGGAAAG TCCCTTATTG	600
244	ATTGGCCAAC	610

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247 (2) INFORMATION FOR SEQ ID NO: 8:  
 249       (i) SEQUENCE CHARACTERISTICS:  
 250           (A) LENGTH: 1649 base pairs  
 251           (B) TYPE: nucleic acid  
 252           (C) STRANDEDNESS: single  
 253           (D) TOPOLOGY: linear  
 255       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 257 CGGCAGCCAG CCTATTCTTT GGCCGGGTG GTGCGAGTGG TCGGCTGGC AGAGTCACG     60  
 259 CTGCTTGGCG CCGCAGGTGA TCCCAGCGTC CACTCCCGGG AGCAGTGATG TTGGGCAACT 120  
 261 CTGCGCCGGG GCCTGCGACC CGCGAGGCGG GCTCGGCGCT GCTAGCATTG CAGCAGACGG 180  
 263 CGCTCCAAGA GGACCAAGGAG AATATCAACC CGGAAAAGGC AGCGCCCGTC CAACAACCGC 240  
 265 GGACCCGGGC CGCGCTGGCG GTACTGAAGT CCGGAAACCC GCAGGGTCTA GCGCAGCAGC 300  
 267 AGAGGCCGAA GACGAGACGG GTTGCACCCC TTAAGGATCT TCCTGTAAAT GATGAGCATG 360  
 269 TCACCGTTCC TCCTTGAAAG GCAAACAGTA AACAGCCTGC GTTCACCATT CATGTGGATG 420  
 271 AAGCAGAAAA AGAACAGTCAG AAGAACAGCAG CTGAATCTCA AAAAATAGAG CGTGAAGATG 480  
 273 CCCTGGCTTT TAATTCAAGCC ATTAGTTTAC CTGGACCCAG AAAACCATTG GTCCCTCTTG 540  
 275 ATATATCCAAT GGATGGTAGT TTGAGTCAC CACATACTAT GGACATGTCA ATTGTATTAG 600  
 277 AAGATGAAAA GCCAGTGAGT GTTAATGAAG TACCAAGACTA CCATGAGGAT ATTACACACAT 660  
 279 ACCTTAGGGA AATGGAGGTT AAATGTAAAC CTTAAAGTGGG TTACATGAAG AAACAGCCAG 720  
 281 ACATCACTAA CAGTATGAGA GCTATCCTCG TGGACTGGTT AGTTGAAGTA GGAGAAGAAAT 780  
 283 ATAAACTACA GAATGAGACC CTGCATTGG CTGTGAACTA CATTGATAAGG TTCCTGTCTT 840  
 285 CCATGTCACT GCTGAGAGGA AAACCTCAGC TTGTGGGCAC TGCTGCTATG CTGTTAGCCT 900  
 287 CAAAGTTGAA AGAAATATAC CCCCCAGAAG TAGCAGAGTT TGTGTACATT ACAGATGATA 960  
 289 CCTACACCAA GAAACAAAGTT CTGAGAATGG AGCATCTAGT TTTGAAAGTC CTTACTTTG 1020  
 291 ACTTAGCTGC TCCAACAGTA AATCAGTTTC TTACCCAATA CTTTCTGCAT CAGCAGCCTG 1080  
 293 CAAACTGCAA AGTTGAAAGT TTGCAATGT TTTTGGGAGA ATTAAGTTG ATAGATGCTG 1140  
 295 ACCCATAACCT CAAGTATTTG CCATCAGTTA TTGCTGGAGC TGCCCTTCAT TTAGCACTCT 1200  
 297 ACACAGTCAC GGGACAAAGC TGGCCTGAAT CATTAAATACG AAAGACTGGA TATACCCCTGG 1260  
 299 AAAGTCTTAA GCCTTGCTC ATGGACCTC ACCAGACCTA CCTCAAAGCA CCACAGCATG 1320  
 301 CACAACAGTC AATAAGAGAA AAGTACAAAA ATTCAAAGTA TCATGGTGT TCTCTCCTCA 1380  
 303 ACCCACCAGA GACACTAAAT CTGTAACAAT GAAAGACTGC CTTTGTTC TAAGATGTAA 1440  
 305 ATCACTCAA GTATATGGTG TACAGTTTT AACTTAGGTT TTTAATTAA CAATCATTTC 1500  
 307 TGAATACAGA AGTTGTGGCC AAGTACAAAT TATGGTATCT ATTACTTTT AAATGGTTTT 1560  
 309 AATTTGTATA TCTTTGTAT ATGTATCTGT CTTAGATATT TGGCTAATTAA TAAGTGGTTT 1620  
 311 TGTTAAAGTA TTAATGATGC CAGCTGCCG 1649  
 314 (2) INFORMATION FOR SEQ ID NO: 9:  
 316       (i) SEQUENCE CHARACTERISTICS:  
 317           (A) LENGTH: 175 base pairs  
 318           (B) TYPE: nucleic acid  
 319           (C) STRANDEDNESS: single  
 320           (D) TOPOLOGY: linear  
 322       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
 324 ACCCACTCGT GAGTCCAACG GTCTTTCTG CAGAAAGGAG GACTTTCCCT TCAGGGGTCT 60  
 326 TTCTGGGGCT CTTACTATAA AAGGGGACCA ACTCTCCCTT TGTCATATCT TGTTCTGAT 120  
 328 GACAAAAAAAT AACACATTGT TAAAATTGTA AAATAAAAC ATGAAATATA AATTA 175  
 331 (2) INFORMATION FOR SEQ ID NO: 10:  
 333       (i) SEQUENCE CHARACTERISTICS:  
 334           (A) LENGTH: 166 base pairs  
 335           (B) TYPE: nucleic acid

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336	(C) STRANDEDNESS: single	
337	(D) TOPOLOGY: linear	
339	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
341	GTTTCGCTCC ACATTCTATCC TTTCTTACTG GGCAGTGATG TTGAGAGCAT CAGGCAGGGT	60
343	ATAATGTTAT GTTGCAGTAA CAAACACCCT CAATATCTCA GTGGCTTAAA ATGACAACGA	120
345	TCTTTTTTTT GTTTGTTGT TTATGCTCTA TATCACCCAG GGATCA	166
348	(2) INFORMATION FOR SEQ ID NO: 11:	
350	(i) SEQUENCE CHARACTERISTICS:	
351	(A) LENGTH: 107 base pairs	
352	(B) TYPE: nucleic acid	
353	(C) STRANDEDNESS: single	
354	(D) TOPOLOGY: linear	
356	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
358	TGCTCTGCC CACATCTGAA CAAGCTAATA AGAAAGCCCG ATGTTCTTTC CTTTGGTGCC	60
360	ATTGGGAAAT TCAAACCATG CACAACCTCTG CCTGTATGAA GGGCGCA	107
363	(2) INFORMATION FOR SEQ ID NO: 12:	
365	(i) SEQUENCE CHARACTERISTICS:	
366	(A) LENGTH: 183 base pairs	
367	(B) TYPE: nucleic acid	
368	(C) STRANDEDNESS: single	
369	(D) TOPOLOGY: linear	
371	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
373	CAACCTTAGC CCCTCTCCTC TTCTTCACGA TGCCATTCTG CCATTTCTGT TTTGTGGTAG	60
375	ACAGGTTGGC CCAGGCACTC TAAGGCCAG GCTGGCACAG GTTGGCCAG GCACTTCAAG	120
377	CCTAAGTCCA TTTACAGTTT CTATTCCATC TCTTCCTAAA GAAGAGGAGA GGGGCTAAGG	180
379	TTG	183
382	(2) INFORMATION FOR SEQ ID NO: 13:	
384	(i) SEQUENCE CHARACTERISTICS:	
385	(A) LENGTH: 92 base pairs	
386	(B) TYPE: nucleic acid	
387	(C) STRANDEDNESS: single	
388	(D) TOPOLOGY: linear	
390	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
392	AAACAAACGT CTTTGGGTAA AATTCTATTT CTTTTAATGT TTTAAATAT TTGTAGTCAC	60
394	TAATTGTAAG TCATATTCCCT CTTTGTCCAG CT	92
397	(2) INFORMATION FOR SEQ ID NO: 14:	
399	(i) SEQUENCE CHARACTERISTICS:	
400	(A) LENGTH: 182 base pairs	
401	(B) TYPE: nucleic acid	
402	(C) STRANDEDNESS: single	
403	(D) TOPOLOGY: linear	
405	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
407	GATGTAATTAA AAGCTGTAGA TGAGGGCTAT CGACTGCCAC CCCCCATGGA CTGCCAGCT	60
409	GCCTTGTATC AGCTGATGCT GGACTGCTGG CAGAAAGACA GGAACAAACAG ACCCAAGTTT	120
411	GAGCAGATTG TTAGTATTCT GGACAAGCTT ATCCGGAATC CCGGCAGCCT GAAGGGATCAT	180
413	CA	182
416	(2) INFORMATION FOR SEQ ID NO: 15:	
418	(i) SEQUENCE CHARACTERISTICS:	
419	(A) LENGTH: 174 base pairs	

**VERIFICATION SUMMARY**

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]